

FIGURE 3. BLAST results of Coiled-Coil regions of GAS 40 with other *Streptococcus* bacteria

3(a) BLAST alignment of amino acid sequence of GAS 40 including the first coiled-coil region with SpA precursor of *Streptococcus gordonii*

```
>gi|25990270|gb|AAC44101.3| streptococcal surface protein A precursor
[Streptococcus gordonii]
      Length = 1575
>ref|NP_268623.1| putative surface exclusion protein [Streptococcus pyogenes]
      Length = 873

Score = 63.2 bits (152), Expect = 5e-11
Identities = 65/293 (22%), Positives = 124/293 (42%), Gaps = 13/293
(4%)

Query: 112 QDQTS DKGTATTA AENAQKQAEIKSDYAKQA---EEIKKTTEAYKKEVEAHQAETDKIN
167
      Q + D+ + T A N + K + ++A + ++KT K E+ K
Sbjct: 33 QVKADDRASGETKASNTHDDSLPKPETIQEAKATIDAVEKTLSSQQAELTELATALTKTT
92

Query: 168 AENKAAEDKYQEDLKAHQAEVEKINTANATAKAEYEAKLAQYQKDLAAVQKANEDSQLDY
227
      AE +++ + KA + E A+++ A+ A++Q++L A + ++Q D
Sbjct: 93 AEINHLKEQQDNEQKALTSAQEIYTNLTASSEETLLAQGAHQREL TATETELHNAQADQ
152

Query: 228 QNKLSAYQAELARVQKANAEAKEAYE--KAVKENTAKNAALQAENEAIKQRNETAKANYD
285
      +K +A + A + A++ E K ++N AK A+ + +AI + +TA N
Sbjct: 153 HSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAITKAAQTANDNTK
212

Query: 286 AAMKQYEADLAAIKKAKEDNDADYQAKLAAYQAELARVQKANADAKAAYEKAVENTAKN
345
      A + E A ++ K +LAA +A LA + + K++ + N
Sbjct: 213 ALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEKEAEL SRLKSSAPSTQDSIVGNN
272

Query: 346 TAIQAEN---EAIKQRNAA---AKATYEAALKQYEADLAAAKKANEDSDADYQ 392
      T + E +K+ A+ A+Y K++ AD AK + + YQ
Sbjct: 273 TMKAPQGYPLEELKKLEASGYIGSASYNYYYKEH-ADQIIAKASPGNQLNQYQ 324
```

FIGURE 3, CONT. BLAST results of Coiled-Coil regions of GAS 40 with other Streptococcus bacteria

3(b) BLAST alignment of amino acid sequence of GAS 40 including the first coiled-coil region with SpB precursor of *Streptococcus gordonii*

>gi|25055226|gb|AAC44102.3| streptococcal surface protein B precursor [Streptococcus gordonii]

Length = 1499

>ref|NP_268623.1| putative surface exclusion protein [Streptococcus pyogenes]

Length = 873

Score = 54.3 bits (129), Expect = 2e-08

Identities = 53/226 (23%), Positives = 98/226 (43%), Gaps = 13/226 (5%)

Query: 111 QDQTS DKGTATTAAENAQKQAEIKSDYAKQA---EEIKKTTEAYKKEVEAHQAETDKIN
166

Q + D+ + T A N + K + ++A + ++KT K E+ K
 Sbjct: 33 QVKADDRASGETKASNTHTDSDLPKPETIQEAKATIDAVEKTLSSQKAELTELATALTKTT
92

Query: 167 AENKAAEDKYQEDLKAHQAEVEKINTANATAKAEYEAKLAQYQKDLAAVQKANEDSQLDY
226

AE +++ + KA + E A+++ A+ A++Q++L A + ++Q D
 Sbjct: 93 AEINHLKEQQDNEQKALTSAQEIYTNLTASSEETLLAQGAHQRELATATETELHNAQADQ
152

Query: 227 QNKLSAYQAELARV--QXXXXXXXXXXXXXXXXXNTAKNAALQAENEAIKQRNETAKANYD
284

+K +A + A + + N AK A+ + +AI + +TA N
 Sbjct: 153 HSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAITKAAQTANDNTK
212

Query: 285 AAMKQYE---ADL---AAIKKAKEDNDADYQAKLAAYQAELARVQ 323

A + E ADL A +KK + A +A LA +AEL+R++
 Sbjct: 213 ALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEKEAELSRK 258

FIGURE 3, CONT. BLAST results of Coiled-Coil regions of GAS 40 with other Streptococcus bacteria

3(c) BLAST alignment of amino acid sequence of GAS 40 including the first coiled-coil region with Surface Protein PspA precursor of *Streptococcus pneumoniae*

>gi| 282335 |pir|A41971 surface protein pspA precursor - Streptococcus pneumoniae
 >ref|NP_268623.1| putative surface exclusion protein [Streptococcus pyogenes]

Length = 873

Score = 48.1 bits (113), Expect = 6e-07
 Identities = 46/200 (23%), Positives = 89/200 (44%), Gaps = 23/200 (11%)

Query: 139 KTKFNTVRAMVVPEPEQLAETK-----KKSEEAKQKAPELTKKLEEAKAKLEE-AEKK
 190

+TK + +P+PE + E K K + K + EL L + A++ E++
 Sbjct: 43 ETKASNTHDDSLPKPETIQEAKATIDAVEKTLSSQQKAELELATALTKTTAEINHLKEQQ
 102

Query: 191 ATEAKQKVDAAEEVAPQAKIAELENQVHRLEQELKEIDSESESEDYAKEGFRAPLQSKLDAK
 250

E K A+E+ + E + + + +E+ +E+E + + + ++ L +
 Sbjct: 103 DNEQKALTSAQEIYTNLTASSEETLLAQGAHQRELTATETELHNAQADQHSKETALSEQ
 162

Query: 251 KAKLS----KLEELSDKIDELDAEIAKLEDQL-----KAAEENNNVEDYFKEGLEKTI
 299

KA +S + ++L +++ + IAKL + KAA+ N+ LEK
 Sbjct: 163 KASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAITKAAQTANDNTKALSSELEKA-
 221

Query: 300 AAKKAELEKTEADLKKAVNE 319

KA+LE +A +KK + E
 Sbjct: 222 ---KADLENQKAKVKKQLTE 238

FIGURE 3, CONT. BLAST results of Coiled-Coil regions of GAS 40 with other Streptococcus bacteria

3(d) BLAST alignment of amino acid sequence of GAS 40 including the second coiled-coil region with SpB precursor of *Streptococcus gordonii*

>gi|23380384|gb|AAN18299.1| immunoreactive protein Se89.9 (fragment)
 [Streptococcus equi]

Length = 210

>ref|NP_268623.1| putative surface exclusion protein [Streptococcus pyogenes]

Length = 873

Score = 173 bits (438), Expect = 4e-45

Identities = 98/209 (46%), Positives = 144/209 (68%)

Query: 1 ESDIVDATRFSTTEIPKSGQVIDRSASIQALTNDIASIKGKIASLESRLADPSSEAEVTA
 60

ES+I + RF+ T I G D + + +++ IA+IKGK++SLE+RL+ EA++ A

Sbjct: 509 ESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGVSSLENRLSAIHQEADIMA
 568

Query: 61 AQAKISQLQHLEAAQAKSHKLDQQVEQLANTKDSLRTQLLAAKEEQAQLKANLDKALAL
 120

AQAK+SQLQ +L + +S L+ QV QL +TK SLRT+LLAAK +QAQL+A D++LA

Sbjct: 569 AQAKVSQQLQGKLASTLKQSDSLNLQVRQLNDTKGSLRTELLAAKAKQAQLEATRDQSLAK
 628

Query: 121 LASSKATLHKLEAAMEEAKARVAGLASQKAQLEDLLAFEKNPNRIELAQEKVAAAKKALA
 180

LAS KA LH+ EA E+A ARV L ++KA L+ L F+ NPNR+++ +E++ K+ LA

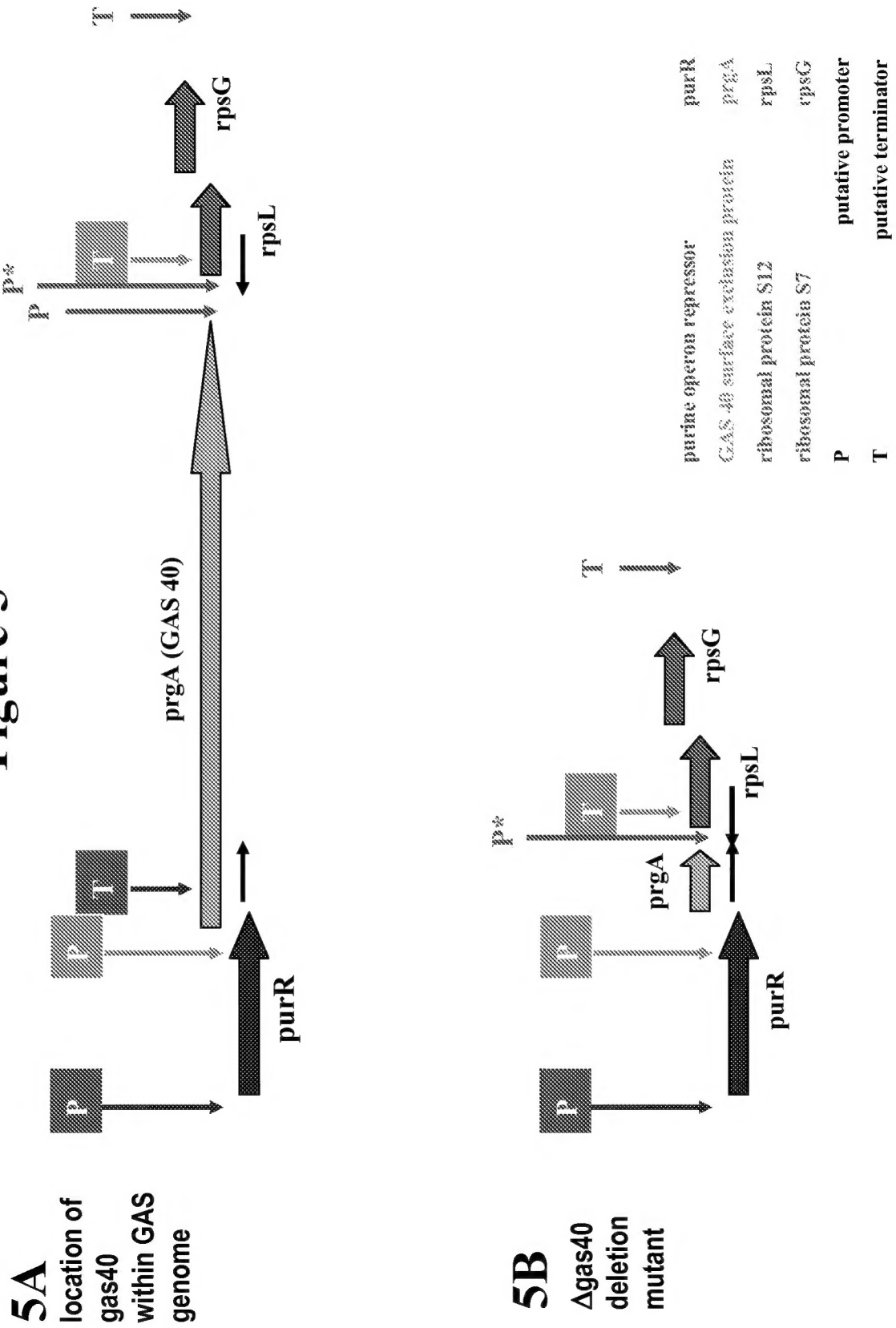
Sbjct: 629 LASLKAALHQTEALAEQAAARVTALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLA
 688

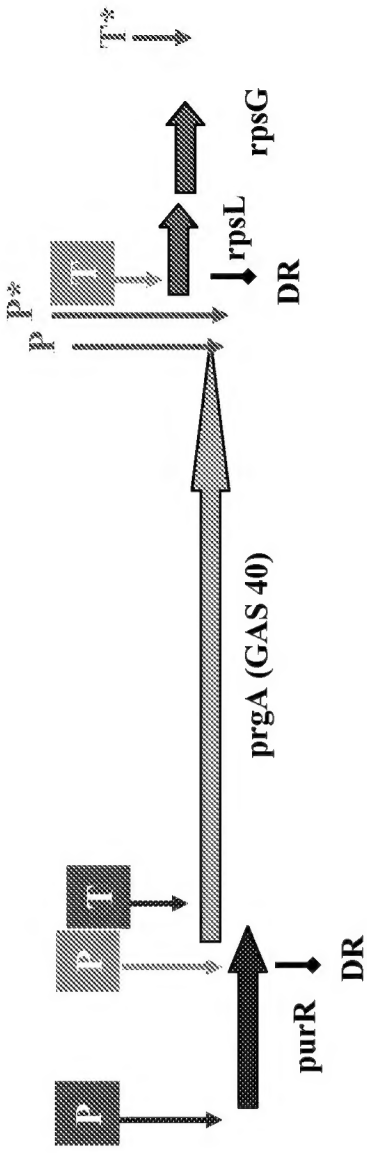
Query: 181 DTEDKLLAAQASLSDLQAQRARLQLSIAT 209

T LL AQ +L+ LQA+++ L+ +IAT

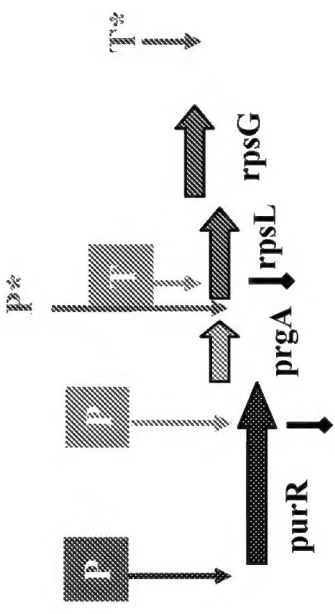
Sbjct: 689 KTTSSLLNAQEALAAALQAKQSSLEATIAT 717

Figure 5

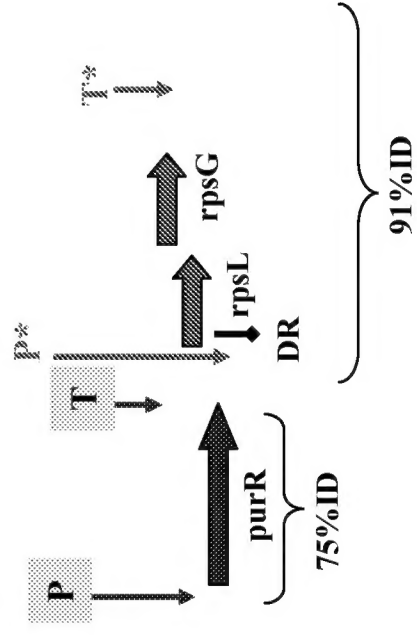




5C
direct repeats
surrounding GAS 40
within wild type genome



5D
location of direct
repeats within Δ *gas40*



5E
corresponding
genomic region
within GBS

Figure 5, cont.